



001560-387.ST25

SEQUENCE LISTING

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Yoshikawa, Takafumi

<120> Genes Encoding Protein Having Citivity of Transferring
Sugar Onto Aurone

<130> 001560-387

<140> US 09/673,300

<141> 2000-10-16

<150> PCT/JP00/00876

<151> 2000-02-16

<150> JP 11-036801

<151> 1999-02-16

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 1751

<212> DNA

<213> Antirrhinum majus

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<222> (1)..(1751)

<223> Nucleotide sequence coding for a protein having glycosyl
transferase to aurone

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<221> CDS

<222> (76)..(1518)

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1 5 10

gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc 159
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr
15 20 25

tca aga ggc ata caa aca aca atc att tcg act ctc gcc ttc gct gat 207
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp
30 35 40

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gtc tta tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu 95 100 105	399
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gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg agc aac ttt Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe 125 130 135 140	495
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gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag Val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu 160 165 170	591
ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr 175 180 185	639
gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly 190 195 200	687
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tcc aag aag cag aat tcg gtt gtt tac gtt tgt ttt gga agt atg gcg	927

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Ser	Gly	Gln	Glu	Phe	Ile	Trp	Val	Val	Lys	Lys	Ala	Lys	Asn	Glu	Glu		
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Lys	Glu	Met	Ala	Arg	Arg	Ala	Val	Glu	Glu	Gly	Gly	Ser	Ser	Tyr	Asn		
445					450					455					460		
ggc	ttg	aat	gag	atg	ata	gag	gat	ttg	agt	gtg	tac	cgt	gct	cca	gaa		1503
Gly	Leu	Asn	Glu	Met	Ile	Glu	Asp	Leu	Ser	Val	Tyr	Arg	Ala	Pro	Glu		
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aaa	caa	gac	tta	aac	tagattctta	tagatgactt	ctagtgtgac	aattgtaatt									1558
Lys	Gln	Asp	Leu	Asn													
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Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys
 35 40 45

Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro
 50 55 60

Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val
 65 70 75 80

Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Leu Gln
 85 90 95

Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val
 100 105 110

Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly
 115 120 125

Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala
 130 135 140

Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp
 145 150 155 160

Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val
 165 170 175

Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe
 180 185 190

Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly
 195 200 205

Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr
 210 215 220

Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu
 225 230 235 240

Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser
 245 250 255

Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln
 260 265 270

Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro
 275 280 285

Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu Ser Gly Gln Glu
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Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly
 305 310 315 320

Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg
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Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His
 340 345 350

Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu
 355 360 365

Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala
 370 375 380

Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly

385 390 395 400
 Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val
 405 410 415
 Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu
 420 425 430
 Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala
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 Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn Gly Leu Asn Glu
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<222> (36)..(1499)

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Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn
10 15 20

101

ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile
25 30 35

149

acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val
40 45 50

197

gat cgg gca gta gtg gca gca cta aag att cag gta gtt cac ctc tat
Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr
55 60 65 70

245

ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac
Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp
75 80 85

293

atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt	341
Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser	
90 95 100	
agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca	389
Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser	
105 110 115	
cca agt tgc ata ata tct gat atg tgt ttt cca tgg aca act aat gtt	437
Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val	
120 125 130	
gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt	485
Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys	
135 140 145 150	
ttt tct tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag	533
Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu	
155 160 165	
tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa	581
Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu	
170 175 180	
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Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp	
185 190 195	
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Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Glu Ala Tyr	
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ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag	725
Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys	
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gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt	773
Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val	
235 240 245	
tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag	821
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265 270 275	
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Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro	
280 285 290	
acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga	965
Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg	
295 300 305 310	
ccc ttt att tgg gtt gtt aga cac aag tca gat gaa ttt aaa agt tgg	1013

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Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu	
330 335 340	
atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att	1109
Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile	
345 350 355	
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Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile	
360 365 370	
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375 380 385 390	
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Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala	
395 400 405	
gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca	1301
Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Glu Lys Val Gly Ala	
410 415 420	
caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc	1349
Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly	
425 430 435	
gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga	1397
Glu Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly	
440 445 450	
gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac	1445
Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Gly Ser Ser His Phe Asn	
455 460 465 470	
ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa	1493
Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys	
475 480 485	
tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacca	1549
Ser Ile	
tctactagag atggttaacaa tccaaactgc gccttttttg cacaataatt attgttttat	1609
gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgccgaact	1669
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 <213> Petunia hybrida

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Gln Arg Gly Val Ile Ile Thr Ile Leu Thr Thr His Phe Asn Ala Thr
 35 40 45

Arg Phe Lys Thr Val Val Asp Arg Ala Val Val Ala Ala Leu Lys Ile
 50 55 60

Gln Val Val His Leu Tyr Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu
 65 70 75 80

Gly Cys Glu Ala Phe Asp Met Leu Pro Ser Met Asp Phe Ala Met Lys
 85 90 95

Phe Phe Asp Ala Thr Ser Arg Leu Gln Pro Gln Val Glu Glu Met Leu
 100 105 110

His Glu Leu Gln Pro Ser Pro Ser Cys Ile Ile Ser Asp Met Cys Phe
 115 120 125

Pro Trp Thr Thr Asn Val Ala Gln Lys Phe Asn Ile Pro Arg Leu Val
 130 135 140

Phe His Gly Met Cys Cys Phe Ser Leu Leu Cys Leu His Asn Leu Arg
 145 150 155 160

Asp Trp Lys Glu Leu Glu Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly
 165 170 175

Leu His Asp Lys Ile Glu Leu Asn Lys Ala Gln Leu Ser Asn Ile Val
 180 185 190

Lys Pro Arg Gly Pro Asp Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys
 195 200 205

Ala Glu Glu Glu Ala Tyr Gly Ile Val Ala Asn Ser Phe Glu Glu Leu
 210 215 220

Glu Pro Glu Tyr Val Lys Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile
 225 230 235 240

Trp Pro Ile Gly Pro Val Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys
 245 250 255

Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu His Gln Cys Leu Lys
 260 265 270

Trp Leu Asp Ser Trp Gly Ala Asn Ser Val Leu Phe Val Cys Leu Gly
 275 280 285

Ser Leu Ser Arg Leu Pro Thr Pro Gln Met Ile Glu Leu Gly Leu Gly
 290 295 300

Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser
 305 310 315 320

Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val
 325 330 335

Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile
 340 345 350

Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn
 355 360 365

Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro
 370 375 380

Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu
 385 390 395 400

Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu
 405 410 415

Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val

420

425

430

Ile Glu Arg Val Met Gly Glu Glu Glu Glu Ala Glu Met Arg Arg Lys
 435 440 445

Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly
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Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu
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Gln Ala Asn Ile Leu Lys Ser Ile
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<210> 9
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 <212> DNA
 <213> Petunia hybrida

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 transferase to aurone

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 Met
 1
 ggt cag ctg cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg 164
 Gly Gln Leu His Phe Phe Phe Phe Pro Met Met Ala His Gly His Met
 5 10 15
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 Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys
 20 25 30
 gcc acc ata atc act act cct ctg aat gaa tca gtt ttc tcc aaa gct 260
 Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala
 35 40 45
 att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa 308
 Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln
 50 55 60 65

gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile 70 75 80	356
cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met 85 90 95	404
caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu 100 105 110	452
gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe 115 120 125	500
aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys 130 135 140 145	548
gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser 150 155 160	596
gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu 165 170 175	644
act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro 180 185 190	692
atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr 195 200 205	740
gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu 210 215 220 225	788
cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu 230 235 240	836
tct ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile 245 250 255	884
tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys 260 265 270	932
cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr 275 280 285	980
gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa	1028

Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln 290 295 300 305	
gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu 310 315 320	1076
gag tgg ttg cct gaa gga ttc gag gaa aga acg aaa gaa aaa ggt cta Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu 325 330 335	1124
att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln Ala 340 345 350	1172
gtg gga gct ttt gtc act cat tgt ggt tgg aat tca acg ctt gaa gga Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly 355 360 365	1220
gta tca gca ggg gtg cct atg gtg acc tgg cct gtg ttt gca gag caa Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln 370 375 380 385	1268
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gag gga ttc aga aac cga gct aaa gcc tac aaa gag atg gca aaa caa Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys Gln 435 440 445	1460
gct att gaa gaa gga gga tct tct tac tct gga ttg act act ttg cta Ala Ile Glu Glu Gly Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu Leu 450 455 460 465	1508
caa gat ata agt aca tat agt tcc aaa agt cat taactgcaca actaaaaaaaa Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His 470 475	1561
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Lys Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys
 35 40 45

Ala Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe
 50 55 60

Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu
 65 70 75 80

Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met
 85 90 95

Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys
 100 105 110

Leu Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys
 115 120 125

Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu
 130 135 140

Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser
 145 150 155 160

Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg
 165 170 175

Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr
 180 185 190

Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser
 195 200 205

Tyr Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val
 210 215 220
 Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro
 225 230 235 240
 Leu Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys
 245 250 255
 Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys
 260 265 270
 Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe
 275 280 285
 Thr Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly
 290 295 300
 Gln Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn
 305 310 315 320
 .
 Glu Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly
 325 330 335
 Leu Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln
 340 345 350
 Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
 355 360 365
 Gly Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu
 370 375 380
 Gln Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala
 385 390 395 400
 Gly Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys
 405 410 415
 Arg Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu
 420 425 430
 Ala Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys

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